

AGATGATGT CCGCGGTGCA AGGTGCAAGT TCGCGGCAT  
 METSerVal GlyArgArg ArgValLysLeu LeuGlyIle  
 1 CCGTATGATG GCAAATGTCT TCATTATTT GATTGTGGA  
 eLeuMETMET AlaAsnValPhe IleTyrLeu IleValGlu  
 2 TCTCTAAA ACAGTAGCCA AGCAAAAAT GGAAGGGG  
 ValSerLysAsn SerSerGln AspLysAsn GlyLysGlyG  
 3 TGTATATAT CCGAAAGAG AGGTCTGCA AGCCACCGG  
 yValIleIle ProLysGlu LysPheTrpLys ProProSe  
 4 CACTCGGGG GCTACTGCA ACAGGGGACA GGAGAAGCTG  
 ThrProArg AlaTyrTrpAsn ArgGluGln GluLysLeu  
 5 ACAGGTGTG ACAAATCGCT CTTCACAGG GTGCGCATC  
 AsnArgProPyr AsnProIle LeuAsnArg ValAlaAsn  
 6 AGACGGGGA GCTAGGCA TCTCAACA CAGTCACTT  
 LysTrpGlyGlu LeuAlaThr SerProAsnThr SerHisLe  
 7 CAGCTATCT CAGCAGACT CCACTGCTT CAGAGCTTG  
 eSerTyrCys GluProAspSer ThrValMET ThrAlaVal  
 8 ACAGATTTA ATAATCTCC GGCAGATTT AAAGCTTTC  
 ThrAspPheAsn AsnLeuPro AspArgPhe LysAspPheL  
 9 TCTGTATTT CAGATCGGG AATTACTGC TCTTATAGA  
 eLeuTyrLeu ArgCysArg AsnTyrSerLeu LeuIleAs  
 10 TCAACCGAG AATGTGCA AGAGCCCTT CTCTATCTG  
 gGlnProLys LysCysAlaLys LysProPhe LeuLeuLeu  
 11 TCGATTAAGT CCGTATTC ACATTTTCC AGAAGGCGAG  
 AlaIleLysSer LeuIlePro HisPheAla ArgArgGlnA  
 12 TATTGCGA GTCTCGGGC CGCAAAACA AGCTAGGGA  
 IleArgGlu SerTrpGly ArgGluThrAsn ValGlyAs  
 13 CCGACAGTA GTGCGGTCT TCTGTGCG CAGACACCC  
 nGlnThrVal ValArgValPhe LeuLeuGly LysThrPro  
 14 CAGAGGACA ACCACCTCA CCGTGGGAC ATGCTTAAGT  
 ProGluAspAsn HisProAsp LeuSerAsp METLeuLysP  
 15 TTGAGGTGA CAGCAACAG CACATCTCA TGTGGACTA  
 heGluSerAsp LysHisGln AspIleLeuMET TrpAsnIy  
 16 TAGAGACA TCTTCAACC TGTCTGAA GGAAGTCTG  
 rArgAspThr PhePheAsnLeu SerLeuLys GluValLeu

FIG. 1 (sheet 1 of 2)

541 TTCTTGGT GGGTGGCA TTTGTGCA GAGCAGGT  
 PheLeuArgTrp ValSerThr SerCysPro AspAlaGluP  
 571 TTGCTTCA GGGGTGAT GAGGTTC TCAACCCA  
 LeuValPheLys GlyAspAsp AspValPheVal AsnThrHi  
 601 TGCATGCT AATTACTCA ATAGCTATC CAAGACAAA  
 sHisIleLeu AsnTyrLeuAsn SerLeuSer LysSerLys  
 631 GCGAAGCT TTTTCATAGG TGGGTGATC CCAATGCTG  
 AlaLysAspLeu PheIleGly AspValIle HisAsnAlaG  
 661 GGGTCAAG GGTAGAAA CTGAGTACT ACATCCAGA  
 LysProHisArg AspLysLys LeuLysTyrTyr IleProGl  
 691 AGTCTTCTC ACGGCTCTT ACGGCTCTA TCGGCTCTT  
 uValPheLys ThrGlyValTyr ProProTyr AlaGlyGly  
 721 GGTGATTC TGTACCTCC GGGGTTC TGCAGCTCT  
 GlyGlyPheLeu TyrSerGly ProLeuAla LeuArgLeuT  
 751 ACAGTCCGC TCGGCTCTC GGTCTCTAC CTATTCATCA  
 yrSerAlaThr SerArgVal HisLeuLysPro IleAspAs  
 781 TTTTCTAC GCAATGCTC TTGAAACT GGGGTCTT  
 pValTyrThr GlyMetCysLeu GluLysLeu GlyLeuVal  
 811 CTGAGAGC ACAAGGCTT GGGCATTT GATATGAG  
 ProGluLysHis LysGlyPhe ArgThrPhe AspIleGluG  
 841 AGAAAAATA GAAAAATTT TTTCTATA TGACCTAT  
 uLysAsnLys LysAsnIle CysSerTyrIle AspLeuME  
 871 GTATGACT AGCGAAGC CTGAGAGT GATGATTC  
 LeuValHis SerArgLysPro GluGluMET IleAspIle  
 901 TGTCTGCT TCGAGTCC TATTAAAA TGTCTA  
 TrpSerGluLeu HisSerPro AsnLeuLys Cys

FIG. 1 (sheet 2 of 2)



YGPYPKPKFESKWTIPKOLYPKVVYPYCSGG

310 320 330

AGEHRDQKLEHYTTEVEFTTGLYPPAGL  
 -CEIRFVRKRRHMERHVDNPPFLLT  
 -S-IFGFHKNHISYOEYRKFPPLLL  
 -SLEPHKESKWTYVSLSEYPPDRWPPVTA  
 NAENENPDSKUYMTPLLYEISERVEVF

GYTFSGDLAERLYKASLHVRLHLLEDVYVG

340 350 360

FLYVPIALHLSSTSRHYPIDT  
 -ALVALIYT  
 -MCGVPPVEMMSKPIKF  
 AFLLQKALROAVLPPFRFDL  
 -V- - - - -KIFVGI

ICLXKLGIDPXXPYG- - -FNHW-KXXKSXC

370 380 390

MQLQKLCLEVEKHKCFRTDIEEANKENIC  
 LERKLEHEFONSC- - - - -PHAYLC  
 -NLKVIHILEDTNLIIFY-RIHLDV  
 VALGASLCHCDD- - -RFHRPAYGPD  
 -TASTRTDVP-PPNEFV- - - - -VSYSC

BYSPVIAVHQP- - -PEEMIRWNL- - -KNL

400 410 420

YIDCLMVSRSR-KQEMDISSQI- - -SPH  
 RRRRVITVNI- - - - -HETWDMSSKH  
 QLRPVIAAGF- - -SKLITTFKQVML- - -RT  
 YSSVIASSHEFGD- - -THVHE- - - - -  
 KYCHLITTS- - - - -QSFLTKYHHQNH

XC- - - - -Y- - - - -

430

K  
 R  
 T  
 C  
 - - - - -H  
 - - - - -RSANY- - - - -A  
 ACANAAKEKAGRYRHRKLH

FIG. 2 (sheet 2 of 2)

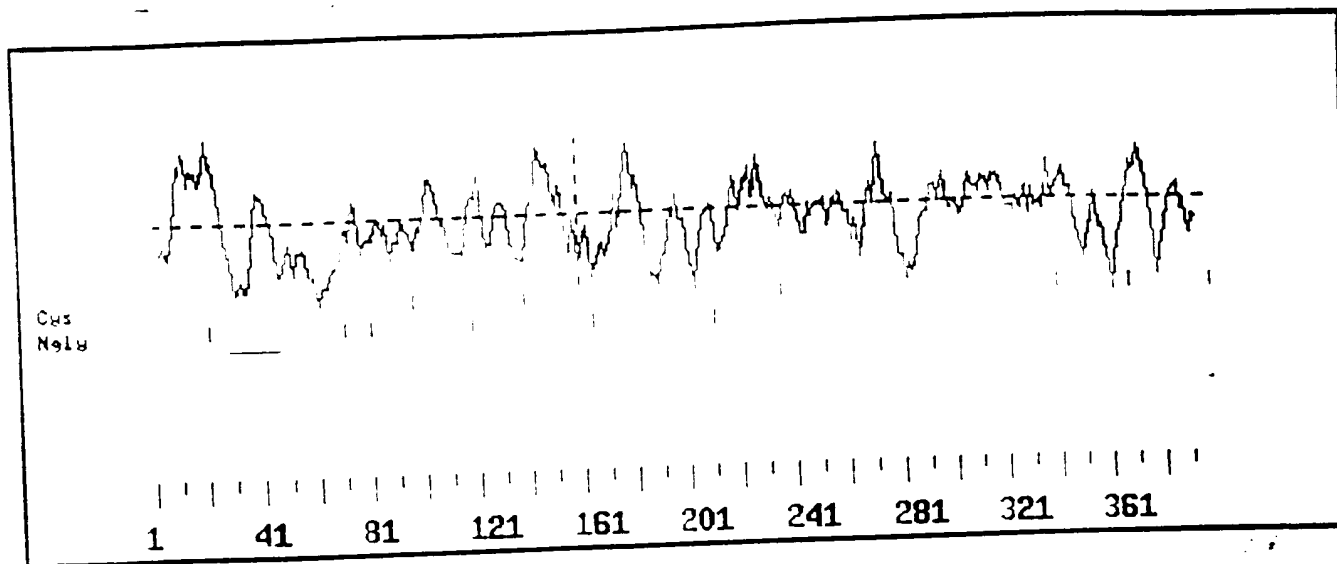


FIG. 3

ATGATTTCGC CTCACGCTTT ACTGGTATT TTAGAAAT  
 METIleCysPro SerAlaLeu LeuValIle LeuArgAsnL  
 11 TAAATACGGG AAAAAAATC ATTCTCAG AGATCCTCA  
 euIleArgGlu GluLysIle IleSerGlnGlu IleLeuAs  
 21 TTGATTGAA TTAGGATGA AAAAGGGAA TATTCAGTTC  
 nLeuIleGlu LeuArgMETLys LysGlyAsn IleGlnLeu  
 31 ACAAACCTCT CAATCAGTGA TGCATTAAA GAAATCGTA  
 ThrAsnSerAla IleSerAsp AlaLeuLys GluIleAspS  
 41 CTAGTGTGCT CAATGTGCTT CTCACCGGG AGACGGGATC  
 erSerValLeu AsnValAla ValThrGlyGlu ThrGlySe  
 51 AGGGAAGTCC AGCTTCATCA ATACCTGAG AGGCATGGG  
 rGlyLysSer SerPheIleAsn ThrLeuArg GlyIleGly  
 61 AATGAGAAG AAGGTGCGC TAAACTGGG CTGTGGGGG  
 AsnGluGluGlu GlyAlaAla LysThrGly ValValGluV  
 71 TACCATCGA AGACATCGA TACAACACC CCATATACC  
 alThrMETGlu ArgHisPro TyrLysHisPro AsnIlePr  
 81 CATGTGGT TTCTGGGAC TCCCTGGAT TGGAGCACA  
 cAsnValVal PheTrpAspLeu ProGlyIle GlySerThr  
 91 AATTCCGAC CAACACTTA CCTGGGAAA ATGAAGTTC  
 AsnPheProPro AsnThrTyr LeuGluLys METLysPheT  
 101 AAGAGTACG TTCTTCATT ATTATTTCG CCGAGGCTT  
 yrGluTyrAsp PhePheIle IleIleSerAla ThrArgPh  
 111 CAGAAAAAT GATATAGCA TTGCAAGC AATCGCATG  
 eLysLysAsn AsnIleAspIle AlaLysAla IleSerMET  
 121 ATGAAGAGG AATCTGCTT CCGGAGACC AAGGTGGAT  
 METLysLysGlu PheTyrPhe ValArgThr LysValAspS  
 131 CTGACATAC AATGAGCA CATGCCAAC CTCAACTT  
 erAspIleThr AsnGluAla AspGlyLysPro GlnThrPh  
 141 TGCAGAGA AAGGTCTCC AGGACCTCC CCTTACTCT  
 eAspLysGlu LysValLeuGln AspIleArg LeuAsnOys  
 151 CTGACACTT TTAGGGGAA TGGCATTCCT GAGGCACAA  
 ValAsnThrPhe ArgGluAsn GlyIleAla GluProProI  
 161 TCTTCTCTT CTCACAAA AATGTTGTC ACTATGACTT  
 lePheLeuLeu SerAsnLys AsnValCysHis TyrAspPh

FIG. 4 (sheet 1 of 2)

581 CCCCCTCCCTC ATGGACAGCC TGTATAGTGA CCCCCTATC  
 eProValLeu METAspLysLeu IleSerAsp LeuProIle  
 591 TCCAGGAGAC ACAATTTTAT CCTCTCCTTA CCCCATAATCA  
 TyrArgArgHis AsnPheMET ValSerLeu ProAsnIleT  
 601 CCGATTCCGT CATTCGAAAG AGCCCCAAT TTCTGAGCA  
 hrAspSerVal IleGluLys LysArgGlnPhe LeuLysGlu  
 611 PGGGTTTGG CCGGAGGGAT TTCTCTCTCA CATTGTGAAT  
 rArgIlePro LeuGluGlyPhe AlaAlaAsp LeuValAsn  
 621 ATCATCCCTT CTCTGACCTT TCTCTTGCAC AGTGATTTCG  
 IleIleProSer LeuIlePhe LeuLeuAsp SerAspLeuG  
 631 AGACTCTCA GAAAGCATG AAATCTCTCC GCHCTGTGTT  
 IleIleLeuLys LysSerMET LysPheTyrArg ThrValPhe  
 641 TCGAGTCCAT GAAACTCTT TCCAGAGATT AGCTAGGGAC  
 eGlyValAsp GluThrSerLeu GluArgLeu AlaArgAsp  
 651 TCGGAATAG AGGTGCTCA GCTGGGGCC ATGATAAAT  
 TrpGluIleGlu ValAspGln ValGluAla METIleLysS  
 661 CTTCTCTCTT CTTCAAACT ACAGATGAG AAACAATACA  
 erProAlaVal PheLysPro ThrAspGluGlu ThrIleGlu  
 671 AGAAGGCTT TCAAGATATA TTCAGGATT CTGTTTCCCT  
 nGluArgLeu SerArgTyrIle GlnGluPhe CysLeuAla  
 681 AATGGTACT TACTTCTTA AATAGTATT CTGAAGAAA  
 AsnGlyTyrLeu LeuProLys AsnSerPhe LeuLysGluI  
 691 TATTCTCTT GAAATATAG TCTCTGACA TCGTCTCTCA  
 LePheTyrLeu LysTyrLys PheLeuAspMET ValThrGlu  
 701 AGATGCTAAA ACTCTCTTA AGAGATATG TTTPAGAAAC  
 AspAlaLys ThrLeuLys GluIleLys LeuArgAsn  
 711 PG

FIG. 4 (sheet 2 of 2)

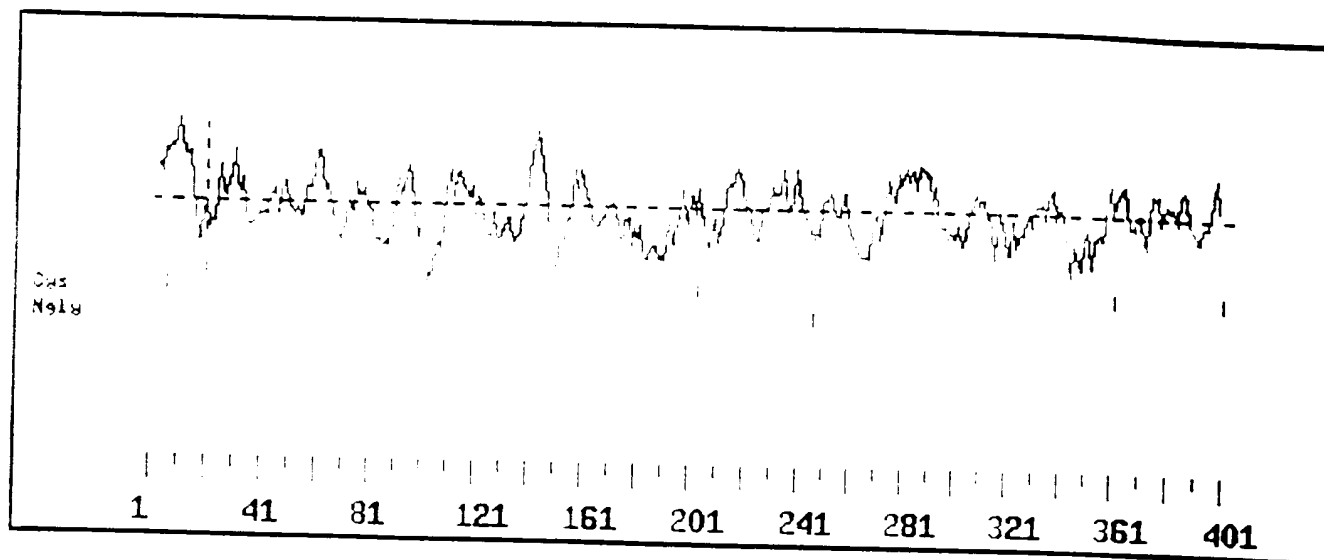


FIG. 5



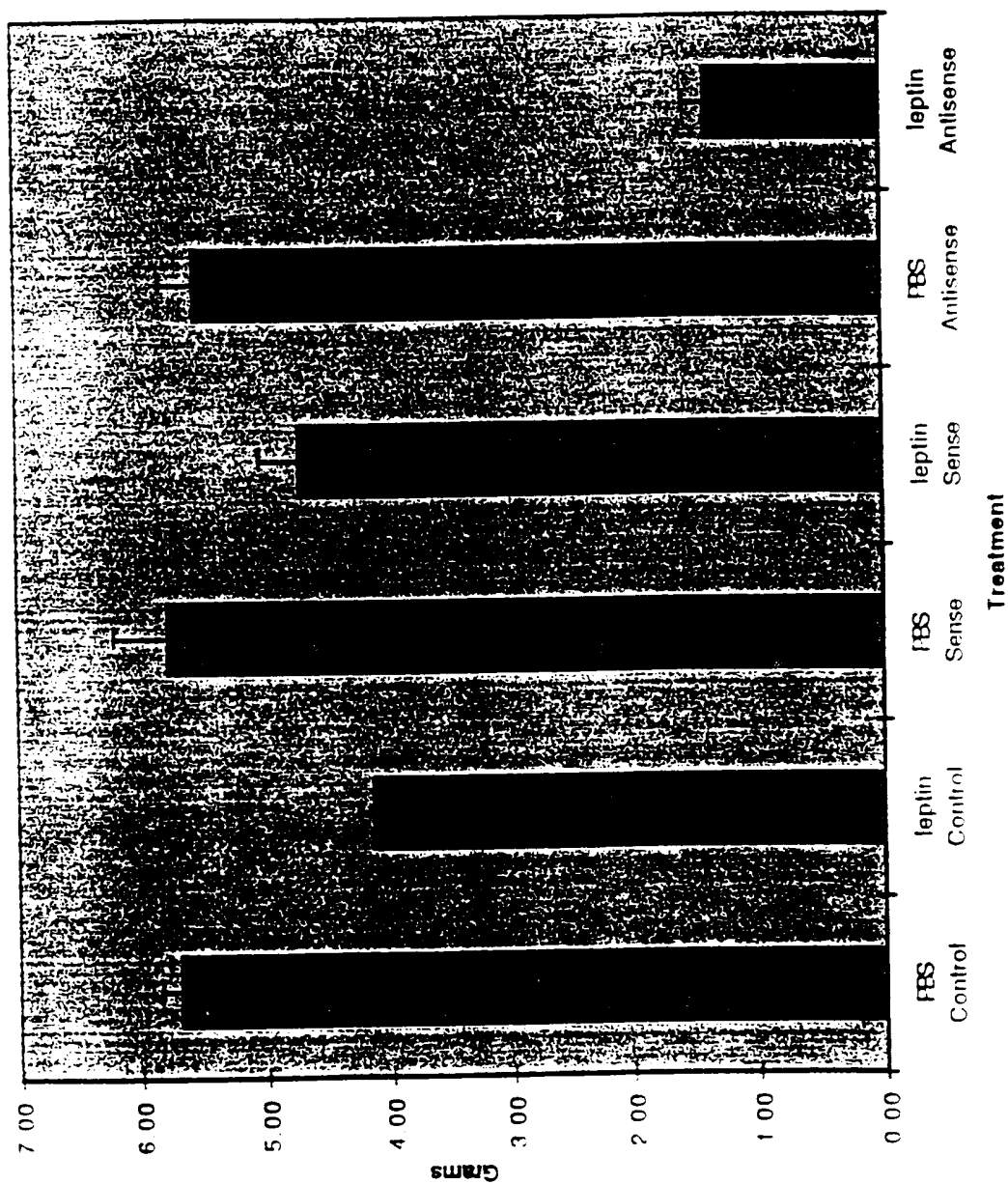


FIG. 6

5'

ACGCGTCCGCGCAGCGGCAGCGGCAGCAGCGGCAACAAGTGCCGGAGGCTA  
GCAGAGCCAAGCCGGAGCAGTCCCTGCCGCCGACACCGCCGGGCGCCCGTC  
CGGGGCGCCGCGCATGGAGCGTGAGCTGCGGCGGTGCGCGGGCTGAGCCGC  
GCGGAGCGGCCGGGACGTGGATGTGGCCGCGATCTCCCGCCCTTGCCCCCGC  
CCCGCCGAGCTGGAGCTGCTCCCGGACAAGATATGAGAA**ATG**AGTGTTGGA  
CGTCGAAGAATAAAGTTGTTGGGTATCCTGATGATGGCAAATGTCTTCATTTA  
TTTTATTATGGAAGTCTCCAAAAGCAGTAGCCAAGAAAAAAATGGAAAAGGG  
GAAGTAATAATACCCAAAGAGAAGTTCTGGAAGATATCTACCCCTCCCGAGG  
CATACTGGAACCGAGAGCAAGAGAAGCTGAACCGGCAGTACAACCCCATCCT  
GAGCATGCTGACCAACCAGACGGGGGAGGCGGGCAGGCTCTCCAATATAAG  
CCATCTGAACTACTGCGAACCTGACCTGAGGGGTCACGTCGGTGGTTACGGGT  
TTTAACAACCTTGCCGGACAGATTTAAAGACTTTCTGCTGTATTTGAGATGCCG  
CAATTATTCACTGCTTATAGATCAGCCGGATAAGTGTGCAAAGAAACCTTTCT  
TGTTGCTGGCGATTAAGTCCCTCACTCCACATTTTGCCAGAAGGCAAGCAATC  
CGGGAATCCTGGGGCCAAGAAAGCAACGCAGGGAACCAAACGGTGGTGCGA  
GTCTTCCTGCTGGGGCCAGACACCCCCAGAGGACAACCACCCCGACCTTTCAG  
ATATGCTGAAATTTGAGAGTGAGAAGCACCAAGACATTCTTATGTGGAACTA  
CAGAGACACTTTCTTCAACTTGTCTCTGAAGGAAGTGCTGTTTCTCAGGTGGG  
TAAGTACTTCCTGCCCAGACACTGAGTTTGTTCCTCAAGGGCGATGACGATGTT  
TTTGTGAACACCCATCACATCCTGAATTACTTGAATAGTTTATCCAAGACCAA  
AGCCAAAGATCTCTTCATAGGTGATGTGATCCACAATGCTGGACCTCATCGG  
GATAAGAAGCTGAAGTACTACATCCCAGAAGTTGTTTACTCTGGCCTCTACCC  
ACCCTATGCAGGGGGAGGGGGGTTCTCTACTCCGGCCACCTGGCCCTGAGG  
CTGTACCATATCACTGACCAGGTCCATCTCTACCCCATTGATGACGTTTATAC  
TGGAATGTGCCTTCAGAACTCGGCCTCGTTCCAGAGAAACACAAAGGCTTC

AGGACATTTGATATCGAGGAGAAAAACAAAAATAACATCTGCTCCTATGTAG  
ATCTGATGTTAGTACATAGTAGAAAACCTCAAGAGATGATTGATATTTGGTCT  
CAGTTGCAGAGTGCTCATTAAAAATGCTAAAAATAGATACAACTCAATTTKG  
SATWGRAAGGGGTWTTTTGRATWGGYCCCATGTTGGGGTCTCACATTAGAGT  
AATTTCTATTTNAANCATGAAATTGCCTTTATGAGTGATACCCATTTANGGCC  
TCTAANCCTTCATTTGNACTCACGTGAAGAAGGGAAAGCGGGAGAAGGTAAT  
TTNTTTATGGTGAATGGCAGGATATTGGTCTGACTTACCGNTAGGGGANTTTA  
AAACTGGNCCTTTTTGAATCTGTTTGGATGGCCCTT

MSVGRRIKLLGILMMANVFIYFIMEVSKSSSQEKNGKGEVIIPKEKFWKISTPPE  
AYWNREQEKLNRQYNPILSMLTNQTGEAGRLSNISHLNYCEPDLRVTSVVTGFN  
NLPDRFKDFLLYLRCRNYSLIDQPDKCAKKPFLLLAIKSLTPHFARRQAIREWG  
QESNAGNQTVVRVFLLGQTPPEDNHPDLSMLKFESEKHQDILMWNRYRDTFFNL  
SLKEVLFLRWVSTSCPDTEFVFKGDDDVFNTHILNYLNSLSKTKAKDLFIGDV  
IHNAGPHRDKKLYYIPEVVYSGLYPPYAGGGGFLYSGHLALRLYHITDQVHLY  
PIDDVYTGMCCLQKLGLVPEKHKGFRTFDIEEKNKNNICSYVDLMLVHSRKPQEM  
IDIWSQLQSAHLKC

START

201 CCCCCCCCCCGGAGCTGGAGCTGCTCCCGGACAAGATATGAGAAATGAGTGTGAGCGT 260  
 5 CCCCCCCCCCGGAGCTGGAGGTGTCCCTAGACAAGGTATGAGAGATGAGTGTGGGGCGT 64  
 261 CGAAGAATAAAGTTGTTGGGTATCCTGATGATGGCAAATGTCTTCATTTATTTTATTATG 320  
 45 CGAAGAGTCAAGTTGCTGGGCATCCTGATGATGGCAAATGTCTTCATTTATTTGATTGTG 124  
 321 GAAGTCTCCAAAAGCAGTAGCCAAGAAAAAATGGAAAAGGGGAAGTAATAATACCCAAA 380  
 125 GAAGTCTCCAAAACAGTAGCCAAGACAAAAAATGGAAAGGGAGGAGTAATAATCCCGAAA 184  
 381 GAGAAGTTCTGGAAGATATCTACCCCTCCCGAGGCATACTGGAACCSAGAGCAAGAGAAG 440  
 185 GAGAAGTTCTGGAAGCCACCCAGCACTCCCGGGGCATACTGGAACAGGGAACAGGAGAAG 244  
 441 CTGAACCSGGCAGTACAACCCCATCCTGAGCATGCTGACCAACCAGACCGGGGAGGCGGGC 500  
 145 CTGAACAGGTGGTACAATCCCATCTTCAACAGGCTGGCCATCCAGACAGGGGAGGTAGCC 304  
 501 AGGCTCTCCAATATAAGCCATCTCAACTACTGCGAACCTGACCTCAGGGTCACGTCCGTG 560  
 105 AATCTCTCCAAACACAAGTCACTGAGCTATTGTGAACCGAGCTCGACGGTCATGACAGCT 364  
 561 GTTACGGGTTTTTAACAACCTTGCCCGACAGATTTAAAGACTTTCTGCTGTATTTGAGATGC 620  
 365 GTGACAGATTTTAATAATCTGCCCGACAGATTTAAAGACTTTCTGCTGTATTTGAGATGC 424  
 621 CGCAATTATTCACTGCTTATAGATCAGCCGGATAAGTGTGCAAAGAAACCTTTCTTGTG 680  
 425 CGGAATTACTCGCTGCTTATAGATCAACCGAAGAAATGTGCAAAGAAGCCCTTCTTACTA 484  
 681 CTGGCGATTAAAGTCCCTCACTCCACATTTTGGCAGAAGGCAAGCAATCCGGGAATCCTGG 740  
 485 TTGGCGATAAAGTCCCTCATTCCACATTTTGGCAGAAGGCAAGCAATTCGGGAGTCTTGG 544  
 741 GGCCAAGAAAGCAACGCAGGGAACCAAACGGTGGTGCGAGTCTTCCTGCTGGGCGAGACA 800  
 545 GGCCGAGAAACCAACGTAGGGAACCAGACAGTAGTGAGGGTCTTCCTGTTGGGCAAGACA 604  
 801 CCCCCAGAGGACAACCACCCCGACCTTTTCAATATGCTGAAATTTGAGAGTGAGAAGCAC 860  
 605 CCCCCAGAGGACAACCACCCCTGACCTTTTGGACATGCTTAAGTTTGAGAGTGACAAGCAC 664  
 861 CAAGACATTCTTATGTGGAACACAGAGACACTTCTTCAACTGTCTCTGAAGGAAGTG 920  
 665 CAGGACATCCTCATGTGGAACATATAGAGACACATTCTTCAACCTGTCCCTGAAGGAAGTG 724  
 921 CTGTTTCTCAGGTGGGTAAAGTACTTCTGCCCAGACACTGAGTTTGTTTTCAAGGGCGAT 980  
 725 CTGTTTCTTAGGTGGGTGAGCACTTCTGTCCAGACGCGAGTTTGTCTTCAAGGGCGAT 784  
 981 CACGATGTTTTTGTGAACACCCATCAGATCCTGAATTAAGTTGAATAGTTTATCCAAGAGC 1040  
 785 GATGACGTGTTTGTGAACACCCATCAGATCCTTAATTACTTGAATAGCTTATCCAAGAGC 844  
 1041 AAAGCCAAAGATCTCTTATAGGTGATGTGATCCCAATGCTGGACCTCATCGGGATAAG 1100  
 845 AAAGCCAAAGACTTGTCTATAGGTGAGTGTGATCCCAATGCTGGGCTCACCGGGATAAG 904

FIG. 9 (10F2)



MSVGRRRIKLLGILMMANVFIYFIMEVSKSSSQEKNGKGEV IIPKEKFWKISTPPEAYWN  
MSVGRRRVKLLGILMMANVFIYLIVEVSKNSSQDKNGKGGV IIPKEKFWKPPSTPRAYWN  
\*\*\*\*\*

REQEKLNRQYNPIELMLTNOTGEAGRLSNISHLNYCEPDLRVTSVVTGFNNLPDRFKDFL  
REQEKLNRWYNPIELNRVANQTGELATSPNTSHLSYCEPDSTVMTAVTDFNNLPDRFKDFL  
\*\*\*\*\*

LYLRCRNYSLIDQPDKCAKKPFLLLAIKSLTPHFARRQAIRESWGQESNAGNQTVVRVF  
LYLRCRNYSLIDQPKKCAKKPFLLLAIKSLIPHFARRQAIRESWGRETNGNQTVVRVF  
\*\*\*\*\*

LLGQTPPEDNHPDLSMDLKFESEKHQDILMWNYRDTFFNLSLKEVLFLRWVSTSCPDTF  
LLGKTPPEDNHPDLSMDLKFESEKHQDILMWNYRDTFFNLSLKEVLFLRWVSTSCPDAEF  
\*\*\*\*\*

VFKGDDDVFNTHHILNYLNSLSKTKAKDLFIGDVIHNAGPHRDKKLYYIPEVVYSGLY  
VFKGDDDVFNTHHILNYLNSLSKSKAKDLFIGDVIHNAGPHRDKKLYYIPEVFYTG  
VY\*\*\*\*\*

PPYAGGGGFLYSGHLALRLYHITDQVHLYPIDDVYTGMC LQKLGLVPEKHKGFRTFDIEE  
PPYAGGGGFLYSGPLALRLYSATSRVHLYPIDDVYTGMC LQKLGLVPEKHKGFRTFDIEE  
\*\*\*\*\*

KNKNNICSYVDLMLVHSRKPQEMIDIWSQLQSAHLKC  
KNKNNICSYIDLMLVHSRKPQEMIDIWSQLQSPNLKC  
\*\*\*\*\*

Fig. 11

